

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Russell, John
Colpitts, Tracey
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASE OF THE BREAST
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6131.US.01
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
(B) TELEFAX: 847/938-2623
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGANCTG	CTTCGAGGAG	GAGCTCATCT	GCNCTATCTG	CCTGCACGTT	TTCGTGGAGC	60
CAGTGCAGCT	GCCGTGCAAA	CACANCTTCT	GCCGGGGCTG	CATCGGCGAG	GCGTGGGCCA	120
AGGACAGCGG	CCTCGTACGC	TGCCCAGAGT	GCAACCAGGC	CTACAACCAG	ANGCCGGGCC	180
TGGAGAAGAA	CCTGAAGCTC	ACCAACATCG	TGGAGAAGTT	CAATGCCCTG	CNCGTGGAGA	240
NGCCGCCGGC	GGCGCTGCAC	TG				262

(2) INFORMATION FOR SEQ ID NO:2:

09250883, 024599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTTTCTGTG	AGCCAGTGCA	GCTGCCGTGC	AAACACAAC	TCTGCCGGGG	CTGCATCGGC	60
GAGGCGTGGG	CCAAGGACAG	CGGCCTCGTA	CGCTGCCCAG	AGTGCAACCA	GGCCNACAAC	120
CAGAAGCCGG	GCCTGGNGAA	GAACCTGAAG	CTCACCAACA	TCGTGGAGAA	GTTCAATGCC	180
CTGCACGTGG	AGAANCCGCC	GGCGGCGCTG	CACTGCGTGT	TCTGCCGCCG	CGGCCCCCGG	240
CTGCCCGCGC	AGAAGGTCTG	CCT				263

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATCGGCGAGG	CGTGGGCCAA	GGACAGCNGC	CTCGTACGCT	GCCCAGAGTG	CAACCAGGCC	60
TACAACCAGA	AGCCGGGCCT	GGAGAAGAAC	CTGAAGCTCA	CCAACATCGT	GGAGAAGTTC	120
AATGCCCTGC	ACGTGGAGAN	GCCGCCGGCN	GCGCTGCACT	GCGTGTCTG	CCGCCGCGGC	180
CCCCCGCTGC	CCGCGCAGAA	GGTCTGCCTG	CGCTGCGAGG	CGCCCTGCTG	CCAGTCCCAC	240
GTGCAGACGC	ACCT					254

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCGCTGCGA	GGCGCCCTGC	TGCCAGTCCC	ACGTGCAGAC	GCACCTGCAG	CAGCCCTCCA	60
CCGCCCCGCG	GCACCTCCTG	GTGGAGGCGG	ACGACGTGCG	GGCCTGGAGC	TGCCCCGAGC	120
ACAACGCCTA	CCGCCTCTAC	CACTGCGAGG	CCGAGCAGGT	GGCCGTGTGC	CAGTACTGCT	180
GCTACTACAG	CGCGCGCAT	CAGGGACACT	CGGTGTGCGA	CGTGGAGATC	CGAAGGAATG	240
AAATCCGGAA	GATGCTCATG	AAGCAGCAGG	ACC			273

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGTGCGAC	GTGGAGATCC	GAAGGAATGA	AATCCGGAAG	ATGCTCATGA	AGCAGCAGGA	60
CCGGCTGGAG	GAGCGAGAGC	AGGACATTGA	GGACCAGCTG	TACAACTCG	AGTCAGACAA	120
GCGCTGGTG	GAGGAGAAAG	TGAACCAACT	GAAGGAGGAA	GTTCCGGCTG	AGTACGAGAA	180
GCTGCACCAG	CTGCTGGACG	AGGACCTGCG	GCAGACAGTG	GAGGTCTTAG	ACAAGGCCCA	240

09250883.021559

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGGAGGAGA	AAGTGAACCA	ACTGAAGGAG	GAAGTTCGGC	TGCAGTACGA	GAAGCTGCAC	60
CAGCTGCTGG	ACGAGGACCT	GCGGCAGACA	GTGGAGGTCC	TAGACAAGGC	CCAGGCCAAG	120
TTCTGCAGCG	AGAACGCAGC	GCAGGCGCTG	CACCTCGGGG	AGCGCATGCA	GGAGGCCAAG	180
AAGCTGCTGG	GCTCCCTGCA	GCTGCTCTTT	GATAAGACGG	AGGATGTCAG	CTTCATGAAG	240
AACACCAAGT	CTGTGAAAAT	CCTGATGG				268

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGAGAACGCA	GCGCAGGCGC	TGCACCTCGG	GGAGCGCATG	CAGGAGGCCA	AGAAGCTGCT	60
GGGCTCCCTG	CAGCTGCTCT	TTGATAAGAC	GGAGGATGTC	AGCTTCATGA	AGAACACCAA	120
GTCTGTGAAA	ATCCTGATGG	ACAGGACCCA	GACCTGCACG	AGCAGCAAGC	CTTTCCCCCA	180
CTAAGATCGG	CCACCTGAAC	TCCAAGCTTT	CCTGAACGAA	TGGCCAAGAA	GGAGAAANCA	239

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAAAATCCTG	ATGGACAGGA	CCCAGACCTG	CACGAGCAGC	AGCCTTTCCC	CCACTAAGAT	60
CGGCCACCTG	AACTCCAAGN	TCT				83

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAAATCCTG	ATGGACAGGA	CCCAGACCTG	CACGAGCAGC	AGCCTTTCCC	CCACTAAGAT	60
CGGCCACCTG	AACTCCAAGC	TCTTCCTGAA	CGAAGGNCCA	AGAAGGAGAA	GCAGCTGCGG	120
AAAATGCTAG	AAGGCCCTT	CAGCAGCCG	GTGCCCTTCC	TGCAGAGTGT	CCCCCTGTAC	180
CCTTGCGGCG	TGAGCAGCTC	TGGGGCGGAA	AAGCGCAAGC	ACTCAACGGC	CTTCCCAGAG	240
GCCAGTTTCC	TAGAGACGTC	GTCGGGCCCT	GTGGGCG			277

(2) INFORMATION FOR SEQ ID NO:10:

09250803 "021599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTGCACGNG CAGCAGCCTT TCCCCCACTA AGATCGGCCA CCTGAACTCC AAGCTCTTCC	60
TGAACGAAGG CCCAAGAAGG AGAAGCAGCT GCGGAAAATG CTAGAAGGCC CCTT	114

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGCACGAG CAGCAGCCTT TCCCCCACTA AGATCGGCCA CCTGAACTCC AAGCTCTTCC	60
TGAACGAATG GCCAAGAAGG AGAAGCAGCT GCGGAAAATG CTAGAAGGCC CCTTCAGCAC	120
GCCGGTGCCC TTCCTGCAGA GTGTCCCCCT GTACCCTTGC GCGGTGAGCA GCTCTGGGGC	180
GGAAAAGCGC AAGCACTCAA CGGCCTTCCC AGAGGCCAGT TTCCTAGAGA CGTCGTCGGG	240
CCCTGTGGGC GGCCAGTACG GGGCGGCGGG CACAGCCAGC GGTGAGGGCC AGT	293

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCCAAGCTC TTCCTGAACG AAGTGTCCAA GAAGGAGAAG CAGCTGCGGA AAATGCTAGA	60
AGGCCCCCTT AGCACGCCGG TGCCCTTCCT GCAGAGTGTC CCCCTGTACC CTTCGNGCGT	120
GAGCAGCTCT GGGGCGGAAA AGCGCAAGCA CTCACGGGCC TTCCAGAGG CCAGTTTCCT	180
AGAGACGTCG TCGGGCCCTG TGGGCGGCCA GTACGGGGCG GCGGGCACAG CCAGCGGT	238

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCCGGTGCC CTTCTGCAG AGTGTCCCCC TGTACCCTTG CCGCGTGANA GCTCTGGGGC	60
GGAAAAGCGC AAGACTCAAC GGCCTTCCCA GAGGCCAGTT TCCTAGAGAC GTCGTCGGGC	120
CCTGTGGGCG GCCAGTACGG GCGGCGGGG ACAGCCAGCG GTGAGGGCCA GTCTGGGCAG	180
CCCCTGGGGC CCTGCAGCTC CACGCAGCAA TTGGTGGCCC TGCCGGGCGG CGCCCAACCA	240
GTGCACTCAA GCCCCGTGTT CCCCCATCG CAGTATCCCA ATGG	284

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs

09250883.024599

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAAGANCTG	CTTCGAGGAG	GAGCTCATCT	GCNCTATCTG	CCTGCACGTT	TTCGTGGAGC	60
CAGTGCAGCT	GCCGTGCAAA	CACAACTTCT	GCCGGGGCTG	CATCGGCGAG	GCGTGGGCCA	120
AGGACAGCGG	CCTCGTACGC	TGCCCAGAGT	GCAACCAGGC	CTACAACCAG	AAGCCGGGCC	180
TGGAGAAGAA	CCTGAAGCTC	ACCAACATCG	TGGAGAAGTT	CAATGCCCTG	CACGTGGAGA	240
AGCCGCCGCG	GGCGCTGCAC	TGCGTGTCT	GCCGCCGCGG	CCCCCGCTG	CCCGCGCAGA	300
AGGTCTGCCT	GCGCTGCGAG	GCGCCCTGCT	GCCAGTCCCA	CGTGCAGACG	CACCTGCAGC	360
AGCCCTCCAC	CGCCCGCGGG	CACCTCCTGG	TGGAGGCGGA	CGACGTGCGG	GCCTGGAGCT	420
GCCCGCAGCA	CAACGCCTAC	CGCCTCTACC	ACTGCGAGGC	CGAGCAGGTG	GCCGTGTGCC	480
AGTACTGCTG	CTACTACAGC	GGCGCGCATC	AGGGACACTC	GGTGTGCGAC	GTGGAGATCC	540
GAAGGAATGA	AATCCGGAAG	ATGCTCATGA	AGCAGCAGGA	CCGGCTGGAG	GAGCGAGAGC	600
AGGACATTGA	GGACCAGCTG	TACAAACTCG	AGTCAGACAA	GCGCCTGGTG	GAGGAGAAAG	660
TGAACCAACT	GAAGGAGGAA	GTTCGGCTGC	AGTACGAGAA	GCTGCACCAG	CTGCTGGACG	720
AGGACCTGCG	GCAGACAGTG	GAGGTCCTAG	ACAAGGCCCA	GGCCAAGTTC	TGCAGCGAGA	780
ACGCAGCGCA	GGCGCTGCAC	CTCGGGGAGC	GCATGCAGGA	GGCCAAGAAG	CTGCTGGGCT	840
CCCTGCAGCT	GCTCTTTGAT	AAGACGGAGG	ATGTCAGCTT	CATGAAGAAC	ACCAAGTCTG	900
TGAAAATCCT	GATGGACAGG	ACCCAGACCT	GCACGAGCAG	CAGCCTTTCC	CCCACTAAGA	960
TCGGCCACCT	GAACTCCAAG	CTCTTCCTGA	ACGAAGGGCC	AAGAAGGAGA	AGCAGCTGCG	1020
GAAAATGCTA	GAAGGCCCCCT	TCAGCACGCC	GGTGCCCTTC	CTGCAGAGTG	TCCCCCTGTA	1080
CCCTTGCGCG	GTGAGCAGCT	CTGGGGCGGA	AAAGCGCAAG	CACTCAACGG	CCTTCCCAGA	1140
GGCCAGTTTC	CTAGAGACGT	CGTCGGGGCC	TGTGGGCGGC	CAGTACGGGG	CGGCGGGCAC	1200
AGCCAGCGGT	GAGGGCCAGT	CTGGGCAGCC	CCTGGGGCCC	TGCAGCTCCA	CGCAGCAATT	1260
GGTGGCCCTG	CCGGGCGGCG	CCCAACCAGT	GCACTCAAGC	CCCGTGTTC	CCCCATCGCA	1320
GTATCCCAAT	GG					1332

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09250883.024699

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Cys	Phe	Glu	Glu	Glu	Leu	Ile	Cys	Ile	Cys	Leu	His	Val	Phe	Val
1				5				10						15	
Glu	Pro	Val	Gln	Leu	Pro	Cys	Lys	His	Asn	Phe	Cys	Arg	Gly	Cys	Ile
			20					25					30		
Gly	Glu	Ala	Trp	Ala	Lys	Asp	Ser	Gly	Leu	Val	Arg	Cys	Pro	Glu	Cys
		35					40					45			
Asn	Gln	Ala	Tyr	Asn	Gln	Lys	Pro	Gly	Leu	Glu	Lys	Asn	Leu	Lys	Leu
50						55					60				
Thr	Asn	Ile	Val	Glu	Lys	Phe	Asn	Ala	Leu	His	Val	Glu	Lys	Pro	Pro
65					70					75					80
Ala	Ala	Leu	His	Cys	Val	Phe	Cys	Arg	Arg	Gly	Pro	Pro	Leu	Pro	Ala
				85					90				95		
Gln	Lys	Val	Cys	Leu	Arg	Cys	Glu	Ala	Pro	Cys	Cys	Gln	Ser	His	Val
			100					105					110		
Gln	Thr	His	Leu	Gln	Gln	Pro	Ser	Thr	Ala	Arg	Gly	His	Leu	Leu	Val
		115					120					125			
Glu	Ala	Asp	Asp	Val	Arg	Ala	Trp	Ser	Cys	Pro	Gln	His	Asn	Ala	Tyr
		130				135					140				
Arg	Leu	Tyr	His	Cys	Glu	Ala	Glu	Gln	Val	Ala	Val	Cys	Gln	Tyr	Cys
145					150					155					160
Cys	Tyr	Tyr	Ser	Gly	Ala	His	Gln	Gly	His	Ser	Val	Cys	Asp	Val	Glu
				165					170					175	
Ile	Arg	Arg	Asn	Glu	Ile	Arg	Lys	Met	Leu	Met	Lys	Gln	Gln	Asp	Arg
			180					185					190		
Leu	Glu	Glu	Arg	Glu	Gln	Asp	Ile	Glu	Asp	Gln	Leu	Tyr	Lys	Leu	Glu
		195					200					205			
Ser	Asp	Lys	Arg	Leu	Val	Glu	Glu	Lys	Val	Asn	Gln	Leu	Lys	Glu	Glu
	210					215				220					
Val	Arg	Leu	Gln	Tyr	Glu	Lys	Leu	His	Gln	Leu	Leu	Asp	Glu	Asp	Leu
225					230					235					240
Arg	Gln	Thr	Val	Glu	Val	Leu	Asp	Lys	Ala	Gln	Ala	Lys	Phe	Cys	Ser
				245					250					255	
Glu	Asn	Ala	Ala	Gln	Ala	Leu	His	Leu	Gly	Glu	Arg	Met	Gln	Glu	Ala
		260						265					270		
Lys	Lys	Leu	Gly	Ser	Leu	Gln	Leu	Leu	Phe	Asp	Lys	Thr	Glu	Asp	
		275				280					285				
Val	Ser	Phe	Met	Lys	Asn	Thr	Lys	Ser	Val	Lys	Ile	Leu	Met	Asp	Arg
	290					295					300				
Thr	Gln	Thr	Cys	Thr	Ser	Ser	Ser	Leu	Ser	Pro	Thr	Lys	Ile	Gly	His
305					310					315				320	
Leu	Asn	Ser	Lys	Leu	Phe	Leu	Asn	Glu	Gly	Pro	Arg	Arg	Arg	Ser	Ser
				325					330					335	
Cys	Gly	Lys	Cys												
			340												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

00250883 021600

Ile Cys Leu His Val Phe Val Glu Pro Val Gln Leu Pro Cys Lys His
 1 5 10 15
 Asn Phe Cys Arg Gly Cys Ile Gly Glu Ala Trp Ala Lys Asp Ser Gly
 20 25 30
 Leu Val Arg Cys Pro Glu Cys Asn Gln
 35 40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Cys Val Phe Cys Arg Arg Gly Pro Pro Leu Pro Ala Gln Lys Val
 1 5 10 15
 Cys Leu Arg Cys Glu Ala Pro Cys Cys Gln Ser His Val Gln Thr His
 20 25 30
 Leu Gln Gln Pro Ser Thr Ala Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Trp Ser Cys Pro Gln His Asn Ala Tyr Arg Leu Tyr His Cys Glu Ala
 1 5 10 15
 Glu Gln Val Ala Val Cys Gln Tyr Cys Cys Tyr Tyr Ser Gly Ala His
 20 25 30
 Gln Gly His Ser Val Cys Asp
 35

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Arg Thr Gln Thr Cys Thr Ser Ser Ser Leu Ser Pro Thr Lys Ile
 1 5 10 15
 Gly His Leu Asn Ser Lys Leu Phe Leu Asn Glu Gly Pro Arg Arg Arg
 20 25 30
 Ser Ser Cys Gly Lys Cys
 35

(2) INFORMATION FOR SEQ ID NO:22:

00250883.021509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
 1 5 10 15
 His His His His His
 20

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